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(57) Abstract <p>The inventors have discovered some striking, and not previously predicted structural similarities and differences between the structure of Novamyl® and the reported structures of CGTases, and based on this they have constructed variants of maltogenic alpha-amylase having CGTase activity and variants of CGTase having maltogenic alpha-amylase activity. Further, on the basis of sequence homology between Novamyl® and CGTases, the inventors have constructed hybrid enzymes with one or more improvements to specific properties of the parent enzymes, using recombinant DNA methodology.</p>			

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AMYLOLYTIC ENZYME VARIANTS

FIELD OF THE INVENTION

The present invention relates to methods of converting a maltogenic alpha-amylase into a cyclodextrin glucanotransferase (CGTase) or vice versa or creating
5 hybrids of the two. The invention also relates to the variants made by the methods.

BACKGROUND OF THE INVENTION

Cyclodextrin glucanotransferase (CGTase, EC 2.4.1.19) and maltogenic alpha-amylase (EC 3.2.1.133) are two classes of glycosylases that degrade starch by hydrolysis of the α -(1,4)-glycosidic bonds, but the initial products are predominantly
10 cyclic for CGTases and linear for the maltogenic alpha-amylase.

Cyclomaltodextrin glucanotransferase (E.C. 2.4.1.19), also designated cyclodextrin glucanotransferase or cyclodextrin glycosyltransferase, abbreviated herein as CGTase, catalyses the conversion of starch and similar substrates into cyclomaltodextrins via an intramolecular transglycosylation reaction, thereby forming
15 cyclomaltodextrins (or CD) of various sizes. Commercially most important are cyclodextrins of 6, 7 and 8 glucose units, termed α -, β - and γ -cyclodextrins, respectively.

CGTases are widely distributed and from several different bacterial sources, including *Bacillus*, *Brevibacterium*, *Clostridium*, *Corynebacterium*, *Klebsiella*,
20 *Micrococcus*, *Thermoanaerobacter* and *Thermoanaerobacterium* have been extensively described in the literature. A CGTase produced by *Thermoanaerobacter* sp. has been reported in Norman B E, Jørgensen S T; *Denpun Kagaku* 1992 39 99-106, and WO 89/03421, and the amino acid sequence has been disclosed in WO 96/33267. The sequence of CGTases from *Thermoanaerobacterium thermosulfurigenes* and from
25 *Bacillus circulans* available on the Internet (SCOP or PDF home pages) as pdf file 1CIU, and the sequence of a CGTase from *B. circulans* is available as pdf file 1CDG.

Tachibana, Y., Journal of Fermentation and Bioengineering, 83 (6), 540-548 (1997) describes the cloning and expression of a CGTase. Variants of CGTases have been described by Kim, Y. H., Biochemistry and Molecular Biology International, 41 (2),
30 227-234 (1997); Sin K-A, Journal of Biotechnology, 32 (3), 283-288 (1994); D Penninga, Biochemistry, 34 (10), 3368-3376 (1995); and WO 96/33267.

Maltogenic alpha-amylase (glucan 1,4- α -maltohydrolase, E.C. 3.2.1.133) is able to hydrolyze amylose and amylopectin to maltose in the alpha-configuration, and is also able to hydrolyze maltotriose as well as cyclodextrin.

35 A maltogenic alpha-amylase from *Bacillus* (EP 120 693) is commercially available under the trade name Novamyl® (product of Novo Nordisk A/S, Denmark) and

is widely used in the baking industry as an anti-staling agent due to its ability to reduce retrogradation of starch (WO 91/04669).

The maltogenic alpha-amylase Novamyl® shares several characteristics with cyclodextrin glucanotransferases (CGTases), including sequence homology (Henrissat B, Bairoch A; Biochem. J., 316, 695-696 (1996)) and formation of transglycosylation products (Christophersen, C., et al., 1997, Starch, vol. 50, No. 1, 39-45).

BRIEF DESCRIPTION OF THE INVENTION

The inventors have discovered some striking, and not previously predicted structural similarities and differences between the structure of Novamyl and the reported structures of CGTases, and based on this they have constructed variants of maltogenic alpha-amylase having CGTase activity and variants of CGTase having maltogenic alpha-amylase activity. Further, on the basis of sequence homology between Novamyl® and CGTases, the inventors have constructed hybrid enzymes with one or more improvements to specific properties of the parent enzymes, using recombinant DNA methodology.

Accordingly, the present invention provides a polypeptide which:

- a) has at least 70 % identity to amino acids 1-686 of SEQ ID NO: 1;
- b) comprises an amino acid modification which is an insertion, substitution or deletion compared to SEQ ID NO: 1 in a region corresponding to amino acids 40-43, 78-85, 136-139, 173-180, 188-195 or 259-268; and
- c) has the ability to form cyclodextrin when acting on starch.

The invention also provides a polypeptide which:

- a) has an amino acid sequence having at least 70 % identity to a parent cyclodextrin glucanotransferase (CGTase);
- b) comprises an amino acid modification which is an insertion, substitution or deletion compared to the parent CGTase in a region corresponding to amino acids 40-43, 78-85, 136-139, 173-180, 188-195 or 259-268 of SEQ ID NO: 1; and
- c) has the ability to form linear oligosaccharides when acting on starch.

Further, the invention provides a method for constructing a maltogenic alpha-amylase, comprising:

- a) recombining DNA encoding a cyclodextrin glucanotransferase (CGTase) and DNA encoding a maltogenic alpha-amylase;
- b) using the recombinant DNA to express a polypeptide; and
- c) testing the polypeptide to select a polypeptide having the ability to form linear oligosaccharides when acting on starch.

Finally, the invention provides a method of selecting DNA encoding maltogenic alpha-amylase in a DNA pool, comprising:

a) amplifying DNA encoding maltogenic alpha-amylase by a polymerase chain reaction (PCR) using primers encoding a partial amino acid sequence of amino acids 1-686 of SEQ ID NO: 1, preferably comprising at least 5 amino acid residues, preferably comprising one or more of positions 188-196, more preferably comprising positions
5 190-194,

b) cloning and expressing the amplified DNA, and

c) screening for maltogenic alpha-amylase activity.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows plasmid pCA31, described in Example 1.

10 Fig. 2 is a diagram showing the shuffling of Novamyl with CGTases, as described in Example 3.

Fig. 3 is a diagram showing the selection of clones with desired features by PCR, as described in Examples 2 and 3.

Fig. 4a-4b shows an alignment of the amino acid sequence of Novamyl (1-686
15 of SEQ ID NO: 1) with the sequence of 3 CGTases as described below.

DETAILED DESCRIPTION OF THE INVENTION

Maltogenic alpha-amylase

The parent maltogenic alpha-amylase used in the invention is an enzyme classified in EC 3.2.1.133. The enzymatic activity does not require a non-reducing end
20 on the substrate and the primary enzymatic activity results in the degradation of amylopectin and amylose to maltose and longer maltodextrins. It is able to hydrolyze amylose and amylopectin to maltose in the alpha-configuration, and is also able to hydrolyze maltotriose as well as cyclodextrin.

A particularly preferred maltogenic alpha-amylase is the amylase cloned from
25 *Bacillus* as described in EP 120 693 (hereinafter referred to as Novamyl). Novamyl has the amino acid sequence set forth in amino acids 1-686 of SEQ ID NO: 1. Novamyl is encoded in the gene harbored in the *Bacillus* strain NCIB 11837 which has the nucleic acid sequence set forth in SEQ ID NO:1.

CGTase

30 The parent CGTase used in the invention is an enzyme classified in EC 2.4.1.19. It may be from any source, e.g. bacterial sources, including *Bacillus*, *Brevibacterium*, *Clostridium*, *Corynebacterium*, *Klebsiella*, *Micrococcus*, *Thermoanaerobacter* and *Thermoanaerobacterium*.

The CGTase preferably has one or more of the following characteristics:

i) an amino acid sequence having at least 50 % identity to amino acids 1-686 of SEQ ID NO: 1, preferably at least 60 %;

ii) being encoded by a DNA sequence which hybridizes at conditions described below to the DNA sequence set forth in SEQ ID NO:1 or to the DNA sequence
5 encoding Novamyl harbored in the *Bacillus* strain NCIB 11837; and

iii) a catalytic binding site comprising amino acid residues corresponding to D228, E256 and D329 as shown in the amino acid sequence set forth in amino acids 1-686 of SEQ ID NO: 1.

Variants of CGTase

10 The CGTase variant of this invention has the ability to form linear oligosaccharides when acting on starch. The starch hydrolysis and the analysis of initial reaction products may be carried out as described in an Example.

The CGTase variant has a modification of at least one amino acid residue in a region corresponding to residues 40-43, 78-85, 136-139, 173-180, 189-195 or 259-268
15 of SEQ ID NO: 1. Each modification may be an insertion, a deletion or a substitution, of one or more amino acid residues in the region indicated. The modification of the parent CGTase is preferably such that the resulting modified amino acid or amino acid sequence more closely resembles the corresponding amino acid or structural region in Novamyl. Thus, the modification may be an insertion of or a substitution with an amino
20 acid present at the corresponding position of Novamyl, or a deletion of an amino acid not present at the corresponding position of Novamyl.

The CGTase variant may particularly comprise an insertion into a position corresponding to the region D190-F194 of Novamyl (amino acid sequence shown in SEQ ID NO: 1). The insertion may comprise 3-7 amino acids, particularly 4-6, e.g. 5
25 amino acids. The insertion may be DPAGF as found in Novamyl or an analogue thereof, e.g. with the first amino acid being negative, the last one being aromatic, and the ones in between being preferably P, A or G. The variant may further comprise a substitution at the position corresponding to T189 of Novamyl with a neutral amino acid which is less bulky than F, Y or W. Other examples of insertions are DAGF, DPGF,
30 DPF, DPAAGF, and DPAAGGF.

Modifications in the region 78-85 preferably include deletion of 2-5 amino acids, e.g. 3 or 4. Preferably, any aromatic amino acid in the region 83-85 should be deleted or substituted with a non-aromatic.

Modifications in the region 259-268 preferably include deletion of 1-3 amino
35 acid, e.g. two. The region may be modified so as to correspond to Novamyl

The CGTase variant may comprise further modifications in other regions, e.g. regions corresponding to amino acids 37-39, 44-45, 135, 140-145, 181-186, 269-273, or 377-383 of Novamyl.

Additional modifications of the amino acid sequence may be modeled on a
 5 second CGTase, i.e. an insertion of or substitution with an amino acid found at a given position in the second CGTase, or they may be made close to the substrate (less than 8 Å from the substrate, e.g. less than 5 Å or less than 3 Å) as described in WO 96/33267.

The following are some examples of variants based on a parent CGTase from
 10 *Thermoanaerobacter* (using *B. circulans* numbering). Similar variants may be made from other CGTases.

L194F+ *194aT+ *194bD+ *194cP+ *194dA+ *194eG+ D196S
 L87H+ D89*+ T91G+ F91aY+ G92*+ G93*+ S94*+ L194F+ *194aT+ *194bD+
 *194cP+ *194dA+ *194eG+ D196S
 15 *194aT+ *194bD+ *194cP+ *194dA+ *194eG+ D196S
 L87H+ D89*+ T91G+ F91aY+ G92*+ G93*+ S94*+ *194aT+ *194bD+ *194cP+
 *194dA+ *194eG+ D196S
 Y260F+ L261G+ G262D+ T263D+ N264P+ E265G+ V266T+ *266aA+
 *266bN+ D267H+ P268V
 20 *194aT+ *194bD+ *194cP+ *194dA+ *194eG+ D196S+ Y260F+ L261G+
 G262D+ T263D+ N264P+ E265G+ V266T+ *266aA+ *266bN+ D267H+ P268V

Variants of Novamyl

The Novamyl variant of this invention has the ability to form cyclodextrin when acting on starch. The starch hydrolysis and the analysis of reaction products may be
 25 carried out as described in an Example.

The Novamyl variant has a modification of at least one amino acid residue in the same regions described above for CGTase variants. However, the modifications are preferably in the opposite direction, i.e. such that the resulting modified amino acid or amino acid sequence more closely resembles the corresponding amino acid or
 30 structural region of a CGTase. Thus, the modification may be an insertion of or a substitution with an amino acid present at the corresponding position of a CGTase, or a deletion of an amino acid not present at the corresponding position of a CGTase.

Preferred modifications include a deletion in the region 190-195, preferably the deletion Δ (191-195) and/or a substitution of amino acid 188 and/or 189, preferably
 35 F188L and/or Y189Y.

Amino acid identity

For purposes of the present invention, the degree of identity may be suitably determined according to the method described in Needleman, S.B. and Wunsch, C.D., (1970), *Journal of Molecular Biology*, 48, 443-45, with the following settings for polypeptide sequence comparison: GAP creation penalty of 3.0 and GAP extension penalty of 0.1. The determination may be done by means of a computer program known such as GAP provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711).

10 The variants of the invention have an amino acid identity with the parent enzyme (Novamyl or CGTase) of at least 70 %, preferably at least 80 %, e.g. at least 90 %, particularly at least 95 % or at least 98 %.

Hybridization

The hybridization referred to above indicates that the analogous DNA
15 sequence hybridizes to the nucleotide probe corresponding to the protein encoding part of the nucleic sequence shown in SEQ ID NO:1, under at least low stringency conditions as described in detail below.

Suitable experimental conditions for determining hybridization at low stringency between a nucleotide probe and a homologous DNA or RNA sequence involves
20 presoaking of the filter containing the DNA fragments or RNA to hybridize in 5x SSC (sodium chloride/sodium citrate, Sambrook, J., Fritsch, E.J., and Maniatis, T. (1989) *Molecular cloning: a laboratory manual*, Cold Spring Harbor Laboratory Press, New York) for 10 min, and prehybridization of the filter in a solution of 5x SSC, 5x Denhardt's solution (Sambrook, et al., *op.cit.*), 0.5% SDS and 100 µg/ml of denatured sonicated
25 salmon sperm DNA (Sambrook, et al., *op.cit.*), followed by hybridization in the same solution containing a random-primed (Feinberg, A. P. and Vogelstein, B. (1983) *Anal. Biochem.* 132:6-13), ³²P-dCTP-labeled (specific activity > 1 x 10⁹ cpm/µg) probe for 12 hours at ca. 45°C. The filter is then washed twice for 30 minutes in 2x SSC, 0.5% SDS at least 55°C (low stringency), more preferably at least 60°C (medium stringency), more
30 preferably at least 65°C (medium/high stringency), more preferably at least 70°C (high stringency), even more preferably at least 75°C (very high stringency).

Molecules which hybridize to the oligonucleotide probe under these conditions are detected by exposure to x-ray film.

Corresponding amino acids

Corresponding amino acids for the following 4 amino acid sequences are shown in the alignment in Fig. 4a-4b which is based on the three-dimensional structure of the sequences.

- 5 1) Novamyl (amino acids 1-686 of SEQ ID NO: 1)
- 2) CGTase from *Thermoanaerobacter thermosulfurigenes* (pdf file 1CIU)
- 3) CGTase from *Thermoanaerobacter*, described in WO 96/33267
- 4) CGTase from *Bacillus circulans* (pdf file 1CDG)

Corresponding amino acid residues in other CGTases may be found by
10 aligning with one of the sequences in Fig. 4a-4b by to the method described in Needleman (*supra*) using the same parameters, e.g. by means of the GAP program (*supra*).

Nomenclature for amino acid modifications

The nomenclature used herein for defining mutations is essentially as
15 described in WO 92/05249. Thus, F188L indicates a substitution of the amino acid F (Phe) in position 188 with the amino acid L (Leu). Δ (191-195) or Δ (191-195) indicates a deletion of amino acids in positions 191-195. 192-A-193 indicates an insertion of A between amino acids 192 and 193. *194aT indicates an insertion of T at the first position after 194. G92* indicates a deletion of G at position 92.

20 Recombination of CGTase and maltogenic alpha-amylase

The present invention further relates to a method for constructing a variant enzyme comprising Novamyl and one or more parent CGTases, wherein said variant has at least one altered property relative to Novamyl and said parent CGTases, which method comprises:

- 25 i) generating DNA fragments encoding amino acid sequences obtainable from Novamyl and said parent CGTases;
- ii) constructing a hybrid variant which contains amino acid sequences generated in step i) by in vivo or in vitro DNA shuffling; and
- iii) testing the resulting variant for said property.

30 The methods for generating DNA fragments referred to in step i) of the method above are well known in the art and may include, for example, treatment of a DNA sequence encoding an amino acid sequence with a restriction enzyme, e.g., DNase I.

The DNA shuffling referred to in step ii) in the method above may be recombination, either *in vivo* or *in vitro*, of nucleotide sequence fragment(s) between
35 two or more polynucleotides resulting in output polynucleotides (i.e., polynucleotides having been subjected to a shuffling cycle) having a number of nucleotide fragments

exchanged, in comparison to the input polynucleotides (i.e. starting point polynucleotides). Shuffling may be accomplished either *in vitro* or *in vivo* by recombination within a cell by methods described in the art (cf., Crameri, et al, 1997, Nature Biotechnology Vol. 15:436-438).

- 5 In a preferred embodiment, at least one DNA fragment obtainable from Novamyl in step i) of the method above encodes an amino acid sequence, which is determined to be of relevance for altering said property.

In a more preferred embodiment, a hybrid variant of a parent CGTase is obtained by the above method comprising a modification of at least one amino acid
10 residue in the group consisting of amino acid residues corresponding to residues 37 to 45, residues 135 to 145, residues 173 to 180, residues 189 to 196, residues 261 to 266, residues 327 to 330, and residues 370 to 376 of SEQ ID NO: 1.

In another more preferred embodiment, a hybrid variant comprising Novamyl and one or more parent CGTases is constructed by the above method in which the
15 amino acid sequence of Asp190-Pro191-Ala192-Gly-193-Phe194 corresponding to the positions in the amino acid sequence shown in SEQ ID NO: 1 is inserted into the corresponding positions in said hybrid, wherein the corresponding positions is determined on the basis of amino acid sequence alignment.

In another more preferred embodiment, a hybrid variant comprising Novamyl
20 and one or more parent CGTase is obtained by the above method in which the amino acid sequence of Asp190-Pro191-Ala192-Gly193-Phe194-Ser195 corresponding to the positions in the amino acid sequence shown in SEQ ID NO: 1 is inserted into the corresponding positions in said hybrid, wherein the corresponding positions is determined on the basis of amino acid sequence alignment.

25 It is possible to use the unique active site loop to select hybrid enzymes with maltogenic alpha-amylase activity from a library of random recombinants. Thus, a maltogenic alpha-amylase and a CGTase may be randomly recombined, e.g. by the DNA shuffling method of Crameri A, et al., op.cit. Those resulting mutants containing the Novamyl loop may be selected using PCR, e.g. as described above in the
30 Examples.

The property to be altered may be substrate specificity, substrate binding, substrate cleavage pattern, specific activity of cleavage, transglycosylation, and relative activity of cyclization.

The DNA sequence encoding a parent CGTase to be used in the methods of
35 the invention may be isolated from any cell or microorganism producing the CGTase in question using methods known in the art.

Cloning a DNA sequence encoding a CGTase

The DNA sequence encoding a parent CGTase may be isolated from any cell or microorganism producing the CGTase in question, using various methods well known in the art, for example, from the *Bacillus* strain NCIB 11837.

- 5 First, a genomic DNA and/or cDNA library should be constructed using chromosomal DNA or messenger RNA from the organism that produces the CGTase to be studied. Then, if the amino acid sequence of the CGTase is known, homologous, labeled oligonucleotide probes may be synthesized and used to identify CGTase-encoding clones from a genomic library prepared from the organism in question. Alternatively, a labeled oligonucleotide probe containing sequences homologous to a known CGTase gene could be used as a probe to identify CGTase-encoding clones, using hybridization and washing conditions of lower stringency.

- Another method for identifying CGTase-encoding clones involves inserting fragments of genomic DNA into an expression vector, such as a plasmid, transforming maltogenic alpha-amylase negative bacteria with the resulting genomic DNA library, and then plating the transformed bacteria onto agar containing a substrate for maltogenic alpha-amylase, thereby allowing clones expressing maltogenic alpha-amylase activity to be identified.

- Alternatively, the DNA sequence encoding the enzyme may be prepared synthetically by established standard methods, e.g. the phosphoroamidite method described by S.L. Beaucage and M.H. Caruthers (1981) or the method described by Matthes et al. (1984). In the phosphoroamidite method, oligonucleotides are synthesized, e.g. in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors.

- 25 Finally, the DNA sequence may be of mixed genomic and synthetic origin, mixed synthetic and cDNA origin or mixed genomic and cDNA origin, prepared by ligating fragments of synthetic, genomic or cDNA origin, wherein the fragments correspond to various parts of the entire DNA sequence, in accordance with techniques well known in the art. The DNA sequence may also be prepared by polymerase chain reaction (PCR) using specific primers, for instance as described in US 4,683,202 or R.K. Saiki et al. (1988).

Random mutagenesis

- A general approach for modifying proteins and enzymes has been based on random mutagenesis, for instance, as disclosed in US 4,894,331 and WO 93/01285. For instance, the random mutagenesis may be performed by use of a suitable physical or chemical mutagenizing agent, by use of a suitable oligonucleotide, or by subjecting the DNA sequence to PCR generated mutagenesis. Furthermore, the random

mutagenesis may be performed by use of any combination of these mutagenizing agents. The mutagenizing agent may, e.g., be one which induces transitions, transversions, inversions, scrambling, deletions, and/or insertions.

Examples of a physical or chemical mutagenizing agent suitable for the present purpose include ultraviolet (UV) irradiation, hydroxylamine, N-methyl-N'-nitro-N-nitrosoguanidine (MNNG), O-methyl hydroxylamine, nitrous acid, ethyl methane sulphonate (EMS), sodium bisulphite, formic acid, and nucleotide analogues. When such agents are used, the mutagenesis is typically performed by incubating the DNA sequence encoding the parent enzyme to be mutagenized in the presence of the mutagenizing agent of choice under suitable conditions for the mutagenesis to take place, and selecting for mutated DNA having the desired properties.

When the mutagenesis is performed by the use of an oligonucleotide, the oligonucleotide may be doped or spiked with the three non-parent nucleotides during the synthesis of the oligonucleotide at the positions which are to be changed. The doping or spiking may be done so that codons for unwanted amino acids are avoided. The doped or spiked oligonucleotide can be incorporated into the DNA encoding the maltogenic alpha-amylase enzyme by any published technique, using e.g. PCR, LCR or any DNA polymerase and ligase as deemed appropriate.

Preferably, the doping is carried out using "constant random doping", in which the percentage of wild-type and mutation in each position is predefined. Furthermore, the doping may be directed toward a preference for the introduction of certain nucleotides, and thereby a preference for the introduction of one or more specific amino acid residues. The doping may be made, e.g., so as to allow for the introduction of 90% wild type and 10% mutations in each position. An additional consideration in the choice of a doping scheme is based on genetic as well as protein-structural constraints. The doping scheme may be made by using the DOPE program (cf., Tomandl, D. et al., 1997, Journal of Computer-Aided Molecular Design 11:29-38; Jensen, LJ, Andersen, KV, Svendsen, A, and Kretzschmar, T (1998) Nucleic Acids Research 26:697-702) which, *inter alia*, ensures that introduction of stop codons is avoided.

When PCR-generated mutagenesis is used, either a chemically treated or non-treated gene encoding a parent CGTase enzyme is subjected to PCR under conditions that increase the misincorporation of nucleotides (Deshler 1992; Leung et al., Technique, Vol.1, 1989, pp. 11-15).

A mutator strain of *E. coli* (Fowler et al., Molec. Gen. Genet., 133, 1974, pp. 179-191), *S. cerevisiae* or any other microbial organism may be used for the random mutagenesis of the DNA encoding the CGTase by, e.g., transforming a plasmid containing the parent CGTase into the mutator strain, growing the mutator strain with

the plasmid and isolating the mutated plasmid from the mutator strain. The mutated plasmid may be subsequently transformed into the expression organism.

The DNA sequence to be mutagenized may be conveniently present in a genomic or cDNA library prepared from an organism expressing the parent CGTase. Alternatively, the DNA sequence may be present on a suitable vector such as a plasmid or a bacteriophage, which as such may be incubated with or otherwise exposed to the mutagenising agent. The DNA to be mutagenized may also be present in a host cell either by being integrated in the genome of said cell or by being present on a vector harbored in the cell. Finally, the DNA to be mutagenized may be in isolated form. It will be understood that the DNA sequence to be subjected to random mutagenesis is preferably a cDNA or a genomic DNA sequence.

In some cases it may be convenient to amplify the mutated DNA sequence prior to expression or screening. Such amplification may be performed in accordance with methods known in the art, the presently preferred method being PCR-generated amplification using oligonucleotide primers prepared on the basis of the DNA or amino acid sequence of the parent enzyme.

Subsequent to the incubation with or exposure to the mutagenising agent, the mutated DNA is expressed by culturing a suitable host cell carrying the DNA sequence under conditions allowing expression to take place. The host cell used for this purpose may be one which has been transformed with the mutated DNA sequence, optionally present on a vector, or one which was carried the DNA sequence encoding the parent enzyme during the mutagenesis treatment. Examples of suitable host cells are the following: gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, *Streptomyces lividans* or *Streptomyces murinus*; and gram negative bacteria such as *E. coli*.

The mutated DNA sequence may further comprise a DNA sequence encoding functions permitting expression of the mutated DNA sequence.

30 DNA shuffling

Alternative methods for rapid preparation of modified polypeptides may be prepared using methods of *in vivo* or *in vitro* DNA shuffling wherein DNA shuffling is defined as recombination, either *in vivo* or *in vitro*, of nucleotide sequence fragment(s) between two or more polynucleotides resulting in output polynucleotides (i.e., polynucleotides having been subjected to a shuffling cycle) having a number of nucleotide fragments exchanged, in comparison to the input polynucleotides (i.e.

starting point polynucleotides). Shuffling may be accomplished either *in vitro* or *in vivo* by recombination within a cell by methods described in the art.

For instance, Weber et al. (1983, Nucleic Acids Research, vol. 11, 5661-5661) describe a method for modifying genes by *in vivo* recombination between two homologous genes, wherein recombinants were identified and isolated using a resistance marker.

Pompon et al., (1989, Gene 83:15-24) describe a method for shuffling gene domains of mammalian cytochrome P-450 by *in vivo* recombination of partially homologous sequences in *Saccharomyces cerevisiae* by transforming *Saccharomyces cerevisiae* with a linearized plasmid with filled-in ends, and a DNA fragment being partially homologous to the ends of said plasmid.

In WO 97/07205 a method is described whereby polypeptide variants are prepared by shuffling different nucleotide sequences of homologous DNA sequences by *in vivo* recombination using plasmid DNA as template.

US patent no. 5,093,257 (Genencor Int. Inc.) discloses a method for producing hybrid polypeptides by *in vivo* recombination. Hybrid DNA sequences are produced by forming a circular vector comprising a replication sequence, a first DNA sequence encoding the amino-terminal portion of the hybrid polypeptide, a second DNA sequence encoding the carboxy-terminal portion of said hybrid polypeptide. The circular vector is transformed into a rec positive microorganism in which the circular vector is amplified. This results in recombination of said circular vector mediated by the naturally occurring recombination mechanism of the rec positive microorganism, which include prokaryotes such as *Bacillus* and *E. coli*, and eukaryotes such as *Saccharomyces cerevisiae*.

One method for the shuffling of homologous DNA sequences has been described by Stemmer (Stemmer, (1994), Proc. Natl. Acad. Sci. USA, Vol. 91, 10747-10751; Stemmer, (1994), Nature, vol. 370, 389- 391; Crameri A, Dawes G, Rodriguez E Jr , Silver S, Stemmer WPC (1997) Nature Biotechnology Vol. 15 , No. 5 pp. 436-438). The method concerns shuffling homologous DNA sequences by using *in vitro* PCR techniques. Positive recombinant genes containing shuffled DNA sequences are selected from a DNA library based on the improved function of the expressed proteins.

The above method is also described in WO 95/22625 in relation to a method for shuffling homologous DNA sequences. An important step in the method described in WO 95/22625 is to cleave the homologous template double-stranded polynucleotide into random fragments of a desired size followed by homologously reassembling of the fragments into full-length genes.

Site-directed Mutagenesis

Once a maltogenic alpha-amylase-encoding DNA sequence has been isolated, and desirable sites for mutation identified, mutations may be introduced using synthetic oligonucleotides. These oligonucleotides contain nucleotide sequences flanking the
5 desired mutation sites; mutant nucleotides are inserted during oligonucleotide synthesis. In a specific method, a single-stranded gap of DNA, bridging the maltogenic alpha-amylase-encoding sequence, is created in a vector carrying the maltogenic alpha-amylase gene. Then the synthetic nucleotide, bearing the desired mutation, is annealed to a homologous portion of the single-stranded DNA. The remaining gap is
10 then filled in with DNA polymerase I (Klenow fragment) and the construct is ligated using T4 ligase. A specific example of this method is described in Morinaga et al. (1984). US 4,760,025 discloses the introduction of oligonucleotides encoding multiple mutations by performing minor alterations of the cassette. However, an even greater variety of mutations can be introduced at any one time by the Morinaga method
15 because a multitude of oligonucleotides, of various lengths, can be introduced.

Another method of introducing mutations into a maltogenic alpha-amylase-encoding DNA sequences is described in Nelson and Long, Analytical Biochemistry 180, 1989, pp. 147-151. It involves a 3-step generation of a PCR fragment containing the desired mutation introduced by using a chemically synthesized DNA strand as one
20 of the primers in the PCR reactions. From the PCR-generated fragment, a DNA fragment carrying the mutation may be isolated by cleavage with restriction endonucleases and reinserted into an expression plasmid.

Localized random mutagenesis

The random mutagenesis may be advantageously localised to a part of the
25 parent CGTase in question. This may, e.g., be advantageous when certain regions of the enzyme have been identified to be of particular importance for a given property of the enzyme, and when modified are expected to result in a variant having improved properties. Such regions may normally be identified when the tertiary structure of the parent enzyme has been elucidated and related to the function of the enzyme.

30 The localized, or region-specific, random mutagenesis is conveniently performed by use of PCR generated mutagenesis techniques as described above or any other suitable technique known in the art. Alternatively, the DNA sequence encoding the part of the DNA sequence to be modified may be isolated, e.g., by insertion into a suitable vector, and said part may be subsequently subjected to
35 mutagenesis by use of any of the mutagenesis methods discussed above.

Expression of maltogenic alpha-amylase variants

The construction of the variant of interest is accomplished by cultivating a microorganism comprising a DNA sequence encoding the variant under conditions which are conducive for producing the variant, and optionally subsequently recovering
5 the variant from the resulting culture broth. This is described in detail further below.

According to the invention, a DNA sequence encoding the variant produced by methods described above, or by any alternative methods known in the art, can be expressed, in the form of a protein or polypeptide, using an expression vector which typically includes control sequences encoding a promoter, operator, ribosome binding
10 site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

The recombinant expression vector carrying the DNA sequence encoding an maltogenic alpha-amylase variant of the invention may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector
15 will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e. a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g. a plasmid, a bacteriophage or an extrachromosomal element, minichromosome or an artificial chromosome. Alternatively, the vector may be one which, when introduced into
20 a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

In the vector, the DNA sequence should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of the DNA sequence encoding a maltogenic alpha-amylase variant of the invention, especially in a bacterial host, are the promoter of the *lac* operon of *E. coli*, the *Streptomyces coelicolor* agarase gene *dagA* promoters, the promoters of the *Bacillus licheniformis* α -amylase gene (*amyL*), the promoters of
30 the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the promoters of the *Bacillus amyloliquefaciens* α -amylase (*amyQ*), the promoters of the *Bacillus subtilis* *xylA* and *xylB* genes, etc. For transcription in a fungal host, examples of useful promoters are those derived from the gene encoding *A. oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *A. niger* neutral α -amylase, *A. niger* acid stable α -amylase,
35 *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase or *A. nidulans* acetamidase.

The expression vector of the invention may also comprise a suitable transcription terminator and, in eukaryotes, polyadenylation sequences operably

connected to the DNA sequence encoding the maltogenic alpha-amylase variant of the invention. Termination and polyadenylation sequences may suitably be derived from the same sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to
5 replicate in the host cell in question. Examples of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the *dal* genes from *B. subtilis* or *B. licheniformis*, or one which confers antibiotic resistance such as ampicillin,
10 kanamycin, chloramphenicol or tetracycline resistance. Furthermore, the vector may comprise *Aspergillus* selection markers such as *amdS*, *argB*, *niaD* and *sC*, a marker giving rise to hygromycin resistance, or the selection may be accomplished by co-transformation, e.g. as described in WO 91/17243.

While intracellular expression may be advantageous in some respects, e.g.
15 when using certain bacteria as host cells, it is generally preferred that the expression is extracellular. In general, the *Bacillus* α -amylases mentioned herein comprise a preregion permitting secretion of the expressed protease into the culture medium. If desirable, this preregion may be replaced by a different preregion or signal sequence, conveniently accomplished by substitution of the DNA sequences encoding the respective
20 preregions.

The procedures used to ligate the DNA construct of the invention encoding maltogenic alpha-amylase variant, the promoter, terminator and other elements, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance,
25 Sambroo, et al., op.cit.).

The cell of the invention, either comprising a DNA construct or an expression vector of the invention as defined above, is advantageously used as a host cell in the recombinant production of a maltogenic alpha-amylase variant of the invention. The cell
30 may be transformed with the DNA construct of the invention encoding the variant, conveniently by integrating the DNA construct (in one or more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of the DNA constructs into the host chromosome may be performed according to conventional
35 methods, e.g. by homologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an insect, but is preferably a microbial cell, e.g. a bacterial or a fungal (including yeast) cell.

Examples of suitable bacteria are gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, or *Streptomyces lividans* or *Streptomyces murinus*, or gram negative bacteria such as *E. coli*. The transformation of the bacteria may, for instance, be effected by protoplast transformation or
10 by using competent cells in a manner known *per se*.

The yeast organism may favorably be selected from a species of *Saccharomyces* or *Schizosaccharomyces*, e.g. *Saccharomyces cerevisiae*. The filamentous fungus may advantageously belong to a species of *Aspergillus*, e.g. *Aspergillus oryzae* or *Aspergillus niger*. Fungal cells may be transformed by a process
15 involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known *per se*. A suitable procedure for transformation of *Aspergillus* host cells is described in EP 238 023.

In a yet further aspect, the present invention relates to a method of producing a maltogenic alpha-amylase variant of the invention, which method comprises cultivating
20 a host cell as described above under conditions conducive to the production of the variant and recovering the variant from the cells and/or culture medium.

The medium used to cultivate the cells may be any conventional medium suitable for growing the host cell in question and obtaining expression of the maltogenic alpha-amylase variant of the invention. Suitable media are available from commercial
25 suppliers or may be prepared according to published recipes (e.g. as described in catalogues of the American Type Culture Collection).

The maltogenic alpha-amylase variant secreted from the host cells may conveniently be recovered from the culture medium by well-known procedures, including separating the cells from the medium by centrifugation or filtration, and precipitating
30 proteinaceous components of the medium by means of a salt such as ammonium sulfate, followed by the use of chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

Screening of variants with maltogenic alpha-amylase activity

Variants produced by any of the methods described above may be tested,
35 either prior to or after purification, for maltogenic alpha-amylase activity, such as amylolytic activity, in a screening assay which measures the ability of the variant to degrade starch. The screening in step 10 in the above-mentioned random mutagenesis

method of the invention may be conveniently performed by use of a filter assay based on the following procedure: A microorganism capable of expressing the variant of interest is incubated on a suitable medium and under suitable conditions for secretion of the variant, the medium being covered with two filters comprising a protein-binding filter placed under a second filter exhibiting a low protein binding capability. The microorganism is grown on the second, top filter. Subsequent to the incubation, the bottom protein-binding filter comprising enzymes secreted from the microorganism is separated from the second filter comprising the microorganism. The protein-binding filter is then subjected to screening for the desired enzymatic activity, and the corresponding microbial colonies present on the second filter are identified. The first filter used for binding the enzymatic activity may be any protein-binding filter, e.g., nylon or nitrocellulose. The second filter carrying the colonies of the expression organism may be any filter that has no or low affinity for binding proteins, e.g., cellulose acetate or Durapore™.

Screening consists of treating the first filter to which the secreted protein is bound with a substrate that allows detection of the amylolytic activity. The enzymatic activity may be detected by a dye, fluorescence, precipitation, pH indicator, IR-absorbance or any other known technique for detection of enzymatic activity. The detecting compound may be immobilized by any immobilizing agent e.g. agarose, agar, gelatine, polyacrylamide, starch, filter paper, cloth; or any combination of immobilizing agents. For example, amylolytic activity can be detected by Cibacron Red labeled amylopectin, which is immobilized in agarose. Amylolytic activity on this substrate produces zones on the plate with reduced red color intensity.

To screen for variants with increased stability, the filter with bound maltogenic alpha-amylase variants can be pretreated prior to the detection step described above to inactivate variants that do not have improved stability relative to the parent CGTase. This inactivation step may consist of, but is not limited to, incubation at elevated temperatures in the presence of a buffered solution at any pH from pH 2 to 12, and/or in a buffer containing another compound known or thought to contribute to altered stability e.g., surfactants, EDTA, EGTA, wheat flour components, or any other relevant additives. Filters so treated for a specified time are then rinsed briefly in deionized water and placed on plates for activity detection as described above. The conditions are chosen such that stabilized variants show increased enzymatic activity relative to the parent after incubation on the detection media.

To screen for variants with altered thermostability, filters with bound variants are incubated in buffer at a given pH (e.g., in the range from pH 2-12) at an elevated temperature (e.g., in the range from 50°-110°C) for a time period (e.g., from 1-20 minutes) to inactivate nearly all of the parent CGTase, rinsed in water, then placed

directly on a detection plate containing immobilized Cibacron Red labeled amylopectin and incubated until activity is detectable. Similarly, pH dependent stability can be screened for by adjusting the pH of the buffer in the above inactivation step such that the parent CGTase is inactivated, thereby allowing detection of only those variants with
5 increased stability at the pH in question. To screen for variants with increased calcium-dependent stability calcium chelators, such as ethylene glycol-bis(β -aminoethyl ether) N,N,N',N'-tetraacetic acid (EGTA), is added to the inactivation buffer at a concentration such that the parent CGTase is inactivated under conditions further defined, such as buffer pH, temperature or a specified length of incubation.

10 The variants of the invention may be suitably tested by assaying the starch-degrading activity of the variant, for instance by growing host cells transformed with a DNA sequence encoding a variant on a starch-containing agarose plate and identifying starch-degrading host cells as described above. Further testing in regard to altered properties, including specific activity, substrate specificity, cleavage pattern,
15 thermoactivation, thermostability, pH dependent activity or optimum, pH dependent stability, temperature dependent activity or optimum, transglycosylation activity, stability, and any other parameter of interest, may be performed on purified variants in accordance with methods known in the art as described below.

The maltogenic alpha-amylase activity of variants of the invention towards
20 linear maltodextrins and cyclodextrins may be assayed by measuring the hydrolysis of maltotriose. Hydrolysis is monitored by the formation of glucose using the GLU-kit (Boehringer Mannheim, Indianapolis IN). Hydrolysis of longer maltodextrins, such as malto-tetraose to -heptaose) and cyclodextrins is monitored by the formation of free reducing ends which is measured spectrophotometrically.

25 Alternatively, amylolytic activity can be assayed using the Phadebas method (BioRad, Inc., Richmond, CA) in which the substrate is a water-insoluble cross-linked starch polymer carrying a blue dye (Phadebas Amylase Test) that is hydrolyzed by amylolytic activity to form water-soluble blue fragments which can then be quantitated spectrophotometrically.

30 In cases where the variants of the invention have been altered in the substrate binding site, it may be desirable to determine whether such variant is capable of performing a transglycosylation reaction, which is described below in Example 1, as is normally observed for CGTases.

Substrate specificity of maltogenic alpha-amylase variants may be assayed by
35 measuring the degree to which such enzymes are capable of degrading starch that has been exhaustively treated with the exoglycosylase β -amylase. To screen for variants which show patterns of degradation on such a substrate differing from the patterns produced by the parent CGTase the following assay is performed: β -limit dextrin is

prepared by incubating 25 ml 1% amylopectin in McIlvane buffer (48.5 mM citrate and 193 mM sodium phosphate pH 5.0) with 24 μ g/ml β -amylase overnight at 30°C. Unhydrolysed amylopectin (i.e., β -limit dextrin) is precipitated with 1 volume 98% ethanol, washed and redissolved in water. 1 ml β -limit dextrin is incubated with 18 μ l enzymes (at 2.2 mg/ml) and 100 μ l 0.2 M citrate-phosphate pH 5.0 for 2 hrs at 30°C and analysed by HPLC as described above. Total hydrolysis of β -limit dextrin is carried out in 2M HCl at 95°C. The concentration of reducing ends is measured by methods known in the art.

Industrial Applications

10 The maltogenic alpha-amylase variants of the invention possess valuable properties which may be advantageously used in various industrial applications. In particular, the enzyme finds potential application for retarding or preventing retrogradation, and thus the staling, of starch based food common in the baking industry.

15 The variant may be used for the preparation of bread and other bread products in accordance with conventional techniques known in the art.

It is believed that the modification of the starch fraction by use of the present invention results in increased volume in baked products and improved organoleptic qualities, such as flavor, mouth feel, palatability, aroma and crust color.

20 The maltogenic alpha-amylase variant may be used as the only enzyme or as a major enzymatic activity in combination with one or more additional enzymes, such as xylanase, lipase, glucose oxidase and other oxidoreductases, or an amylolytic enzyme.

The enzyme variants of the invention also find industrial applicability as a component in washing, dishwashing and hard-surface cleaning detergent compositions. Some variants are particularly useful in a process for the manufacture of linear oligosaccharides, or in the production of sweeteners and ethanol from starch, and/or for textile desizing. Conditions for conventional starch conversion processes, including starch liquefaction and/or saccharification processes, are described in, e.g., US 3,912,590 and in EP patent publications Nos. 252,730 and 63,909.

30 The variants of the invention also find application in processes for the manufacture of cyclodextrins for various industrial applications, particularly in the food, cosmetic, chemical, agrochemical and pharmaceutical industries.

Therefore in another aspect the invention provides maltogenic alpha-amylase variants for use in a process for the manufacture of cyclodextrins, in particular α -, β -, γ -, δ -, ϵ -, and/or ζ -cyclodextrins. In a more preferred embodiment, the invention provides maltogenic alpha-amylase variants for use in a process for the manufacture of α -, β - and γ -cyclodextrins, or mixtures hereof.

In yet another preferred embodiment, the variants of the invention may be used for *in situ* generation of cyclodextrins. In this way the variants of the invention may be added to a substrate containing medium in which the enzyme variants are capable of forming the desired cyclodextrins. This application is particularly well suited for use in methods of producing baked products as described above, in methods for stabilizing chemical products during their manufacture, and in detergent compositions.

Cyclodextrins have an inclusion ability useful for stabilization, solubilization, etc. Thus cyclodextrins can make oxidizing and photolytic substances stable, volatile substances non-volatile, poorly-soluble substances soluble, and odoriferous substances odorless, etc. and thus are useful to encapsulate perfumes, vitamins, dyes, pharmaceuticals, pesticides and fungicides. Cyclodextrins are also capable of binding lipophilic substances such as cholesterol, to remove them from egg yolk, butter, etc.

Cyclodextrins also find utilization in products and processes relating to plastics and rubber, where they have been used for different purposes in plastic laminates, films, membranes, etc. Also, cyclodextrins have been used for the manufacture of biodegradable plastics.

EXAMPLES

The invention is further illustrated with reference to the following examples which are not intended to be in any way limiting to the scope of the invention as claimed.

Example 1: Construction of variants of *Thermoanaerobacter* CGTase with altered substrate specificity

This example describes the construction of CGTase variants with modified substrate specificity. The variants are derived from a parent *Thermoanaerobacter* sp. CGTase (i.e. the wild type), obtained as described in WO 89/03421 and WO 96/33267.

Bacterial strains, plasmids and growth conditions

Escherichia coli ME32 was used for recombinant DNA manipulations. The variants were expressed in SHA273, a derivative of *Bacillus subtilis* 168 which is apr⁻, npr⁻, amyE⁻, amyR2⁻ and prepared by methods known in the art. pCA31-wt is a *E. coli*-*B. subtilis* shuttle vector harboring the parent *Thermoanaerobacter* CGTase, shown in Fig. 1.

DNA manipulations

DNA manipulations and transformation of *E. coli* were essentially as described in Sambrook, J., Fritsch, E.J., and Maniatis, T. (1989) *Molecular cloning: a laboratory*

manual, Cold Spring Harbor Laboratory Press, New York. *B. subtilis* was transformed using methods known in the art.

Site-directed mutagenesis

5 Mutant CGTase genes were constructed via SOE-PCR method (Nelson and Long, *op.cit.*) using the Pwo DNA polymerase (Boehringer Mannheim, Indianapolis, IN). The primary PCR reactions were carried out with the mutagenesis primers 1 and 2 (SEQ ID NO: 3 and 4) plus an upstream or a downstream primer (SEQ ID NO: 5 or 6) on the template strand, respectively. The reaction products were subsequently used as
10 template in a second PCR reaction together with the upstream and downstream primers. The product of the last reaction was digested with *StyI* and *SpeI*, and exchanged with the corresponding fragment (640 bp) from the vector pCA31-wt or pCA31-Δ(87-94) (*T-CGTase* + L82H+D84*+T84bG+F84cY+G84d*+G85*+S86*). The resulting variant plasmids were transformed into *E. coli* ME32 and vector DNA was
15 purified from *E. coli* colonies using the DNA-purification kit from QIAGEN (Qiagen, Inc. Germany). The mutant vectors were finally transformed into *B. subtilis* SHA273 for enzyme expression.

The degeneration of mutagenesis primer 2 (SEQ ID NO: 4) containing A or C/G gave rise to two different amino acid sequences. Thus, two variants of a parent
20 CGTase were constructed. Successful mutations resulted in restriction sites (*Sac I*) at positions 7-12 of SEQ ID NO: 3 and positions 2-7 of SEQ ID NO: 4, which allowed quick screening of transformants. Mutations were verified by standard DNA sequencing techniques. The correctness of the *StyI-SpeI* fragment obtained by PCR was also confirmed by DNA sequencing.

25

Production and purification of CGTase proteins

Enzymes were produced in transformed SHA273 cells grown in shakeflasks at 30-37°C in 2*TY media containing 10 µg/l kanamycin. After 68-72 h of growth the culture was pelleted and the supernatant separated from the cells by centrifugation.
30 After filtration through a 0.45µm nitrocellulose filter, the supernatant was directly applied to an α-cyclodextrin-sepharose-6FF affinity column (Monma et al. 1988 *Biotechnol. Bioeng.* 32, 404-407). After washing the column with 10 mM sodium acetate (pH 5.5), the variants were eluted with the same buffer supplemented with 1% (w/v) α-cyclodextrin. Purity and molecular weight of the variants obtained were checked by
35 SDS-PAGE. Protein concentrations were determined by measuring the absorption at 280 nm using a theoretical extinction coefficient at 1.74 ml/mg⁻¹/cm⁻¹.

Enzyme assays

All assays were performed at pH 6.0 and 37°C. The assay for cyclization activity was performed as described by Penninga et al (1995, *Biochemistry* 34:3368-3376). Starch liquefying activity was measured using the Phadebas Amylase Test kit (Pharmacia A/B, Sweden). Transglycosylation activity was assayed in which 2.2 µM of the variant was incubated with 200 mM maltotriose at 40°C in 10 mM NaOAc pH 5.0 and 1 mM CaCl₂. At different time intervals, aliquots were analyzed by HPLC to measure formation of different maltodextrins. Analytical separations of maltodextrins were performed on a Dionex CarboPac PA1-column connected to a Beckman Gold HPLC-system and a pulsed-amperometric detector. The gradient was 0-600 mM NaOAc over 15 minutes in 0.1 M NaOH. Transglycosylation activity was detected as an increase in the size of the from three to greater than three glucose units covalently linked.

15 **Example 2: Specific PCR amplification using Novamyl-specific PCR primers**

Comparison of Novamyl with CGTases reveals that it is thus far unique in one structural feature: the insertion of a 5 amino acid "loop" in domain A, residues 190 to 194 in the amino acid sequence shown in SEQ ID NO: 1, that affects the enzyme structure near the active site. It is therefore valuable to have a method of obtaining variants with a similar active site structure, especially with respect to the Novamyl active site loop. Here we describe such a method using PCR primers specific to the Novamyl loop to amplify from natural sources only those clones with this unique structural feature.

Step 1. PCR amplification of glycosylases with degenerate primers

25 Alignment of amino acid sequences for Novamyl with known CGTases reveals regions of high homology that can be used to design degenerate oligonucleotide primers for use in the PCR amplification of CGTases from a mixed pool of genomic or cDNA. The resulting fragments of a predicted size range can then be used as template DNA in further PCR amplifications with Novamyl loop-specific primers as described in Step 2.

Alignment of 10 amino acid sequences most related to Novamyl was used to identify two regions of high local homology for the design of degenerate primers: Primer 1 (SEQ ID NO: 7) corresponding to amino acids 88-93 from SEQ ID NO: 1 and Primer 2 (SEQ ID NO: 8) corresponding to amino acids 417-412 from SEQ ID NO: 1.

35 Use of these primers on DNA fragments from bacterial sources can, when used as primers in a PCR reaction under standard conditions, amplify a DNA fragment

approximately 1,000 basepairs in length containing the central core of related glycosylases. Resulting PCR fragments could then be used as templates in step 2, as described below.

Step 2. PCR amplification using Novamyl loop-specific primers (Fig. 3)

- 5 The following primer pair can be used, corresponding to the degenerate translation of the amino acid sequence in the coding (d3, SEQ ID 9) or noncoding (d4, SEQ ID NO: 10) DNA strand:

Primer d3 (SEQ ID NO: 9): degenerate sense primer corresponding to amino acids 190-194 from SEQ ID NO: 1.

- 10 Primer d4 (SEQ ID NO: 10): degenerate anti-sense primer corresponding to amino acids 194-190 from SEQ ID NO: 1.

Alternatively, it is possible to use the degenerate or exact nucleotide sequence of Novamyl through eight amino acids that contain the Novamyl sequence, Phe188-Thr189-Asp190-Pro191-Ala192-Gly193-Phe194-Ser195 (loop underlined) in both DNA

- 15 strands as primers in a PCR reaction:

Primer d5 (SEQ ID NO: 11): degenerate sense primer corresponding to amino acids 188-193 from SEQ ID NO: 1.

Primer d6 (SEQ ID NO: 12): degenerate anti-sense primer corresponding to amino acids 195-190 from SEQ ID NO: 1.

- 20 Primer 7 (SEQ ID NO: 13): Exact Novamyl sense primer corresponding to amino acids 188-193 from SEQ ID NO: 1.

Primer 8 (SEQ ID NO: 14): Exact Novamyl anti-sense primer corresponding to amino acids 195-190 from SEQ ID NO: 1.

- Using the PCR products of step 1 as templates in a PCR reaction together with
25 primer pairs 1 and d4, 2 and d4, 1 and d5, 2 and d6, 1 and 7, or 2 and 8, only those DNA sequences encoding the Novamyl loop are expected to produce DNA fragments of approximately the predicted size (Figure 1, step 2.). Templates lacking the loop-encoding DNA will not produce a product under standard PCR conditions with an annealing temperature of 58°C.

Product	Primer pair	approximate size of product
A1	1 + d4	321
A2	1 + d6	324
A3	1 + 8	324
B1	2 + d3	684

B2	2 + d5	690
B3	2 + 7	690

Step 3. Reconstruction of full-length fragments

Step 2 yields partial coding sequences of glycosylases that contain the Novamyl loop at either the 3' (A fragments) or 5' ends (B fragments) of the DNA fragments. Reassembly of longer clones containing the loop will require the combining of the A and B fragments by SOE-PCR methods known in the art.

Example 3: Conversion of CGTases into Novamyl-like enzymes by random re-combination

10 In this example, the unique active site loop was used to select hybrid enzymes with maltogenic alpha-amylase activity from a library of random recombinants. In this method, Novamyl and the cyclic maltodextrin glucosyl transferase (CGTase) from *Bacillus circulans*, were randomly recombined by the DNA shuffling method of Cramer
A, et al., op.cit. Those resulting mutants containing the Novamyl loop were selected
15 using PCR as described above in Example 2.

Step 1. PCR amplification and shuffling of Novamyl and CGTase (Fig. 2)

Specific oligonucleotide primers specific for either the Novamyl coding sequence or the CGTase coding sequenced were designed as shown in SEQ ID NO: 15-20.

20 The entire Novamyl coding sequence (lacking the signal sequence) was amplified using the Novamyl-specific primer pair #9 and #10 (SEQ ID NO: 15 and 16). Similarly, the mature CGTase coding sequence was amplified using the CGTase-specific primer pair #11 and #12 (SEQ ID NO: 17 and 18). Both amplifications were performed using the following reaction conditions: 100 µM each primer, 0.2 mM each of
25 dATP, dCTP, dGTP, and TTP, 2.5 U AmpliTaq polymerase (Perkin Elmer, Inc.), and 1X concentration of the buffer supplied by the manufacturer. PCR was performed in a Perkin Elmer Thermocycler, model 2400, with the following conditions: 5 minutes at 94 C. 25 cycles of 30 seconds at 94 C., 1 minute at 58 C, and 2 minutes at 72 C. followed by a final incubation of 7 minutes at 72°C.

30 The resulting PCR products were then subjected to DNA shuffling as described by Stemmer et al.. Briefly, the two DNA fragments were mixed in equimolar amounts and randomly digested using DNase I treatment to generate gene fragments of between 50 and 500 bp. These gene fragments were then allowed to anneal to one

another and extend in a PCR reaction under low stringency conditions, resulting in a re-assembling of an intact gene pool containing the reassemble parental DNAs as well as chimeras between the parents. Final amplification of shuffled products was performed using the general primer pair #13 and #14 (SEQ ID NO: 19 and 20) using the PCR
5 conditions described above. Using these primers, all full-length species, both parental and chimeric, were amplified.

Step 2. PCR amplification using Novamyl loop-specific primers (Fig. 3)

Those genes within this mixture containing the Novamyl loop were then selected for as described in Example 2 using the loop-specific primers. In the first round
10 of amplification, the 5' and 3' ends of the genes containing the loop were amplified by using the general primers in combination with the loop specific primers # 7 and #8 (SEQ ID NO: 13 and 14) to amplify either the 5' ends of the genes extending to the loop-encoding sequence #13 and #8 (SEQ ID NO: 19 and 14) or the sequence extending from the loop to the 3' ends of the genes #7 and #14 (SEQ ID NO: 13 and
15 20). As described in Example 2, the resulting fragments were then assembled using SOE PCR to create full-length genes. These products were then selectively amplified using primer pairs lacking a Novamyl-specific primer to produce only chimeras: #11, #10 and #12 (SEQ ID NO: 17, 16 and 18) or #10, #9 and #11 (SEQ ID NO: 16, 15 and 17). In this way, only those clones that contained either the CGTase 5' end and the
20 Novamyl loop or the CGTase 3' end and the Novamyl loop were selected.

The final PCR product were then digested with the enzymes Xba I and Mlu I and inserted into a vector containing an intact signal sequence. The resulting clones were transformed into *Bacillus*, and the resulting polypeptides were sequenced.

3 polypeptides obtained by this method were found to be hybrids containing an
25 N-terminal sequence from Novamyl and a C-terminal sequence from the *B. circulans* CGTase as follows:

Novamyl amino acids 1-196 + CGTase amino acids 198-685

Novamyl amino acids 1-230 + CGTase amino acids 232-685

Novamyl amino acids 1-590 + CGTase amino acids 596-685.

30 These results demonstrate that the method is effective for generating and selecting hybrids containing the

Example 4: Construction of a variant of Novamyl with CGTase activity

A variant of Novamyl was constructed that has an altered substrate specificity relative to the parent enzyme, in which the variant has a CGTase-like
35 transglycosylation/cyclization activity not detectable in the parent enzyme. The variant differs from the parent Novamyl with the amino acid sequence shown in amino acids 1-

686 of SEQ ID NO: 1 in that residues 191-195 were removed, Phe188 was substituted with Leu and Thr189 was substituted with Tyr, termed Δ (191-195)-F188L-T189Y. The variant was constructed by sequence overlap extension PCR (SOE PCR) essentially as described by Nelson and Long (*op.cit.*). SOE PCR consists of two primary PCR that
5 produce two overlapping PCR fragments, both bearing the same modification(s). In a second round of PCR, the two products from the two primary PCR are mixed without addition of template DNA.

Oligonucleotide primers used in the construction of Δ (191-195)-F188L-T189Y:

Mutagenic Primer 1 (SEQ ID NO: 21) and Primer 2 (SEQ ID NO: 22). Positions
10 16-21 of SEQ ID NO: 21 and positions 4-9 of SEQ ID NO: 22 are restriction sites.

The Δ (191-195)-F188L-T189Y were obtained using oligomers A82 (SEQ ID NO: 23) and B346 (SEQ ID NO: 24) as end-primers.

DNA manipulations, transformation of *Bacillus subtilis*, and purification of the resulting variant was performed as described above in Example 4. The final purified
15 variant was analysed for the ability to form cyclodextrin from linear starch and compared to the parent Novamyl enzyme as described below.

Detection of β -cyclodextrin

The variant and the parent Novamyl enzyme were diluted with 10 mM citrate buffer pH 6.0 in order to obtain an equivalent protein concentration prior to assay.

20 The cyclisation reaction mixture in a final volume of 1 ml contained:
0-50 μ l enzyme or variant diluted in 10mM sodium citrate buffer pH 6.0
500 μ l 10%(w/v) Paselli SA2 (AVEBE, Foxhol, The Netherlands) dissolved in 10 mM citrate buffer pH 6.0 for a final solution of 5%

The reaction mixture was pre-incubated in a 50°C water bath for 10 min. before
25 adding the enzyme or variant, and at one-min time intervals a 100 μ l sample was put on ice for further analysis.

β -cyclodextrin was quantitated on the basis of formation of a stable colourless inclusion complex with phenolphthalein; thus, the colour of the solution decreases with as the amount of β -cyclodextrin detected increases.

30 To each of the 100 μ l samples from the cyclization reaction 900 μ l of a working solution (3ml of 3.75 mM phenolphthalein added to 100ml 0.2 M Na₂CO₃, pH 9.7) was added, and the absorbance immediately read at 552 nm. β -cyclodextrin was quantitated on the basis of a calibration curve prepared in a final volume of one-ml as follows:

35 0-50 μ l 2mM β -cyclodextrin (0-100nmol)
50-0 μ l milli-Q water
900 μ l working solution

50 μ l 10% Paselli SA2

A new calibration curve was made for each new preparation of Paselli SA2 solution.

The results of the cyclization assay are presented in the table below as β -cyclodextrin formation (mmol/mg enzyme) for the variant Δ (191-195)-F188L-T189Y and for the parent enzyme, Novamyl:

Time (min)	Variant	Novamyl
0	0	0
2	160	0
3	230	0
4	240	0
5	320	0
6	380	0
7	390	0
8	500	0
10	680	0

The results clearly demonstrate that the variant, unlike the parent Novamyl enzyme, can form β -cyclodextrin.

Example 5: Construction of a CGTase variant with ability to form linear oligo-saccharides

This example describes the construction of a CGTase variant derived from a parent *Thermoanaerobacter* CGTase.

15 Mutant CGTase genes were constructed via SOE-PCR method as described in Example 1. The primary PCR reactions were carried out with the mutagenesis primers A91 (SEQ ID NO: 26) and A90 (SEQ ID NO: 25) plus an upstream or a downstream primer (SEQ ID NO 5 or 6) on the template strand, respectively. The product of the last reaction was digested with Bst1107 I and Pst I, and exchanged with the corresponding
20 fragment (250 bp) from the vector pCA31-wt or pCA31-(T-CGTase + F189L+*190D+*191P+*192A+*193G+*194F+D195S). Successful mutations resulted in restriction sites (Xma I) at positions 4-9 of A91 (SEQ ID NO: 26) and positions 11-16 of

A90 (SEQ ID NO: 25), which allowed quick screening of transformants. The following mutations were verified by standard DNA sequencing techniques:

Y260F+ L261G+ G262D+ T263D+ N264P+ E265G+ V266T+ *266aA+
*266bN+ D267H+ P268V

5 *194aT+ *194bD+ *194cP+ *194dA+ *194eG+ D196S+ Y260F+ L261G+
G262D+ T263D+ N264P+ E265G+ V266T+ *266aA+ *266bN+ D267H+ P268V

Example 6: Properties of CGTase variant with ability to form linear oligosaccharides

Inhibition of starch retrogradation

10 The first variant prepared in Example 5 was tested for its ability to inhibit starch retrogradation was tested as follows:

730 mg of 50 % (w/w) amylopectin slurry in 0.1 M sodium acetate, at a selected pH (3.7, 4.3 or 5.5) was mixed with 20 µl of an enzyme sample, and the mixture was incubated in a sealed ampoule for 1 hour at 40°C, followed by incubation at 100 °C for
15 1 hour in order to gelatinize the samples. The sample was then aged for 7 days at room temperature to allow recrystallization of the amylopectin. A control without enzyme was included.

After aging, DSC was performed on the sample by scanning from 5°C to 95°C at a constant scan rate of 90°C/hour. The area under the first endothermic peak in the
20 thermogram was taken to represent the amount of retrograded amylopectin, and the relative inhibition of retrogradation was taken as the area reduction (in %) relative to the control without enzyme.

The result was a relative inhibition of 21 %.

Reaction pattern with starch

25 The variant was compared with Novamyl and with *Thermoanaerobacter* CGTase by determining the reaction products formed after 24 hours incubation in 5% (w/v) amylopectin using 50 mM sodium acetate, 1 mM CaCl₂, pH 5.0 at 50 °C. The reaction products (in % by weight) were identified and quantitated using HPLC.

Oligosaccharide	Novamyl	CGTase	Variant
G10	-	-	0.7
G9	-	-	1.5
G8	-	-	2.4
G7	-	-	1.9

G6/ α -CD	-	53.9	23.1
G5	-	-	6.1
G4	-	-	8.1
G3/ γ -CD	-	12.0	14.5
G2	97.9	-	11.5
G1	2.1	-	6.8
β -CD		34.1	23.1

The results show clearly that whereas the parent CGTase exclusively forms cyclodextrins, the reaction pattern of the variant has been changed to form both cyclodextrins and linear maltodextrins as initial products.

CLAIMS

1. A polypeptide which:
 - a) has at least 70 % identity to amino acids 1-686 of SEQ ID NO: 1;
 - b) comprises an amino acid modification which is an insertion, substitution or
5 deletion compared to SEQ ID NO: 1 in a region corresponding to amino acids
40-43, 78-85, 136-139, 173-180, 189-195 or 259-268; and
 - c) has the ability to form cyclodextrin when acting on starch.
2. The polypeptide of claim 1 wherein the modification comprises a substitution
with or insertion of the amino acid residue present at the corresponding position of a
10 cyclodextrin glucanotransferase (CGTase) and/or deletion of an amino acid residue
which is not present at that position in a cyclodextrin glucanotransferase (CGTase).
3. The polypeptide of claim 1 or 2 wherein the CGTase is derived from a strain of
Bacillus, *Brevibacterium*, *Clostridium*, *Corynebacterium*, *Klebsiella*, *Micrococcus*,
Thermoanaerobacter or *Thermoanaerobacterium*.
- 15 4. The polypeptide of any of claims 1-3 wherein the modification comprises a de-
letion in the region 190-195, preferably the deletion Δ (191-195).
5. The polypeptide of any of claims 1-4 which further comprises a substitution of
amino acid 188 and/or 189, preferably F188L and/or Y189Y.
6. A method of constructing a variant of a parent maltogenic alpha-amylase,
20 which method comprises:
 - a) modifying the amino acid sequence by an insertion, substitution or dele-
tion in a region corresponding to amino acids 40-43, 78-85, 136-139, 173-180,
189-195 or 259-268 of SEQ ID NO: 1;
 - b) optionally modifying the amino acid sequence by an insertion, substitu-
25 tion or deletion at a position other than a);
 - c) optionally repeating a) - b) recursively;
 - d) preparing the variant resulting from a) - c);

- e) testing the variant by hydrolyzing starch and analyzing the initial products;
 - f) optionally repeating a) - e) recursively; and
 - g) selecting a variant having the ability to form cyclodextrin from starch.
- 5 7. A polypeptide which:
- a) has an amino acid sequence having at least 70 % identity to a parent cyclodextrin glucanotransferase (CGTase);
 - b) comprises an amino acid modification which is an insertion, substitution or deletion compared to the parent CGTase in a region corresponding to
10 amino acids 40-43, 78-85, 136-139, 173-180, 189-195 or 259-268 of SEQ ID NO: 1; and
 - c) has the ability to form linear oligosaccharides as an initial product when acting on starch.
8. The polypeptide of claim 7 wherein the modification comprises a substitution
15 with or insertion of the amino acid residue present at the corresponding position of SEQ ID NO: 1 and/or deletion of an amino acid residue which is not present at that position in SEQ ID NO: 1.
9. The polypeptide of claim 7 or 8, wherein the modification is an insertion of the amino acid sequence DPAGF (Asp-Pro-Ala-Gly-Phe) at a position corresponding to
20 D190-F194 of SEQ ID NO: 1.
10. The polypeptide of any of claims 7-9, wherein the CGTase is derived from a strain of *Bacillus*, *Brevibacterium*, *Clostridium*, *Corynebacterium*, *Klebsiella*, *Micrococcus*, *Thermoanaerobacter* or *Thermoanaerobacterium*.
11. The polypeptide of any of claims 7-10, which further comprises a modification
25 in a region corresponding to amino acids 37-39, 44-45, 135, 140-145, 181-186, 269-273, or 377-383 of SEQ ID NO: 1.

12. A method of constructing a variant of a parent cyclodextrin glucanotransferase (CGTase), which method comprises:
- a) modifying the amino acid sequence by an insertion, substitution or deletion in a region corresponding to amino acids 40-43, 78-85, 136-139, 173-180, 189-195 or 259-268 of SEQ ID NO: 1;
 - b) optionally modifying the amino acid sequence by an insertion, substitution or deletion at a position other than a);
 - c) optionally repeating a) - b) recursively;
 - d) preparing the variant resulting from a) - c);
 - e) testing the variant by hydrolyzing starch and analyzing the initial products;
 - f) optionally repeating a) - e) recursively; and
 - g) selecting a variant having the ability to form linear oligosaccharides as an initial product from starch.
13. A nucleic acid sequence encoding the polypeptide of any of claims 1-5 or 7-11, preferably operably linked to one or more control sequences which direct the expression of the variant in a suitable expression host.
14. A recombinant expression vector comprising the nucleic acid sequence of claim 13, a promoter, and transcriptional and translational stop signals, and preferably further comprising a selectable marker.
15. A transformed host cell comprising the nucleic acid sequence of claim 13 or the vector of claim 14.
16. A method for producing the polypeptide of any of claims 1-5 or 7-11, comprising:
- a) cultivating a host cell comprising a nucleic acid construct comprising a nucleic acid sequence encoding said variant under conditions conducive to expression of the variant; and
 - b) recovering the variant.
17. A method for constructing a maltogenic alpha-amylase, comprising:

- a) recombining DNA encoding a cyclodextrin glucanotransferase (CGTase) and DNA encoding a maltogenic alpha-amylase;
- b) using the recombinant DNA to express a polypeptide; and
- c) testing the polypeptide to select a polypeptide having the ability to form linear oligosaccharides when acting on starch.

18. The method of claim 17, further comprising amplifying the recombinant DNA with primers encoding a partial amino acid sequence of amino acids 1-686 of SEQ ID NO: 1 in combination with primers encoding a partial sequence of the CGTase, said primers preferably comprising at least 5 amino acid residues, more preferably comprising one or more of positions 188-196, most preferably comprising positions 190-194.

19. The method of claim 17 or 18, wherein the primers encoding a partial sequence of SEQ ID NO: 1 comprise a partial sequence of the DNA sequence shown in SEQ ID NO: 1.

20. The method of any of claims 17-19, wherein the mature forms of the CGTase and the maltogenic alpha-amylase have at least 40% identity, preferably at least 50%, more preferably at least 60%.

21. The method of any of claims 17-20, wherein the CGTase is derived from a strain of *Bacillus*, *Brevibacterium*, *Clostridium*, *Corynebacterium*, *Klebsiella*, *Micrococcus*, *Thermoanaerobacter* or *Thermoanaerobacterium*.

22. A method of selecting DNA encoding maltogenic alpha-amylase in a DNA pool, comprising:

- a) amplifying DNA encoding maltogenic alpha-amylase by a polymerase chain reaction (PCR) using primers encoding a partial amino acid sequence of amino acids 1-686 of SEQ ID NO: 1, preferably comprising at least 5 amino acid residues, preferably comprising one or more of positions 188-196, more preferably comprising positions 190-194,
- b) cloning and expressing the amplified DNA, and

- c) screening for maltogenic alpha-amylase activity.

23. A process for preparing a dough or a baked product prepared from the dough which comprises adding the polypeptide of any of claims 7-11 or a variant constructed by the method of any of claims 12 or 17-20 to the dough in an amount which
5 is effective to retard the staling of the bread.

24. A process for preparing cyclodextrin, comprising treating liquefied starch with the polypeptide of any of claims 1-5 or the variant constructed by the method of claim
6.

25. A method for producing a variant, comprising:
10 a) constructing the variant by the method of claim 6 or 12;
b) transforming a microorganism with a DNA sequence encoding the variant;
c) cultivating the transformed microorganism under conditions which are conducive for producing the variant, and
d) recovering the variant from the resulting culture broth.

1/5

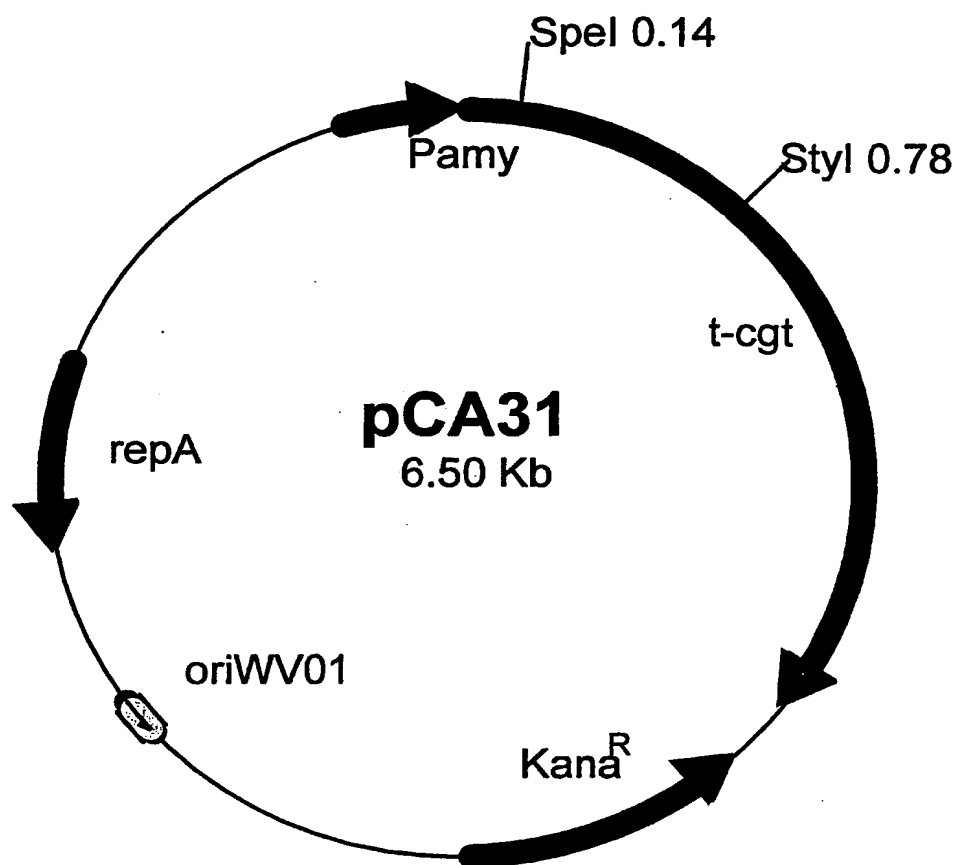


Fig. 1

2/5

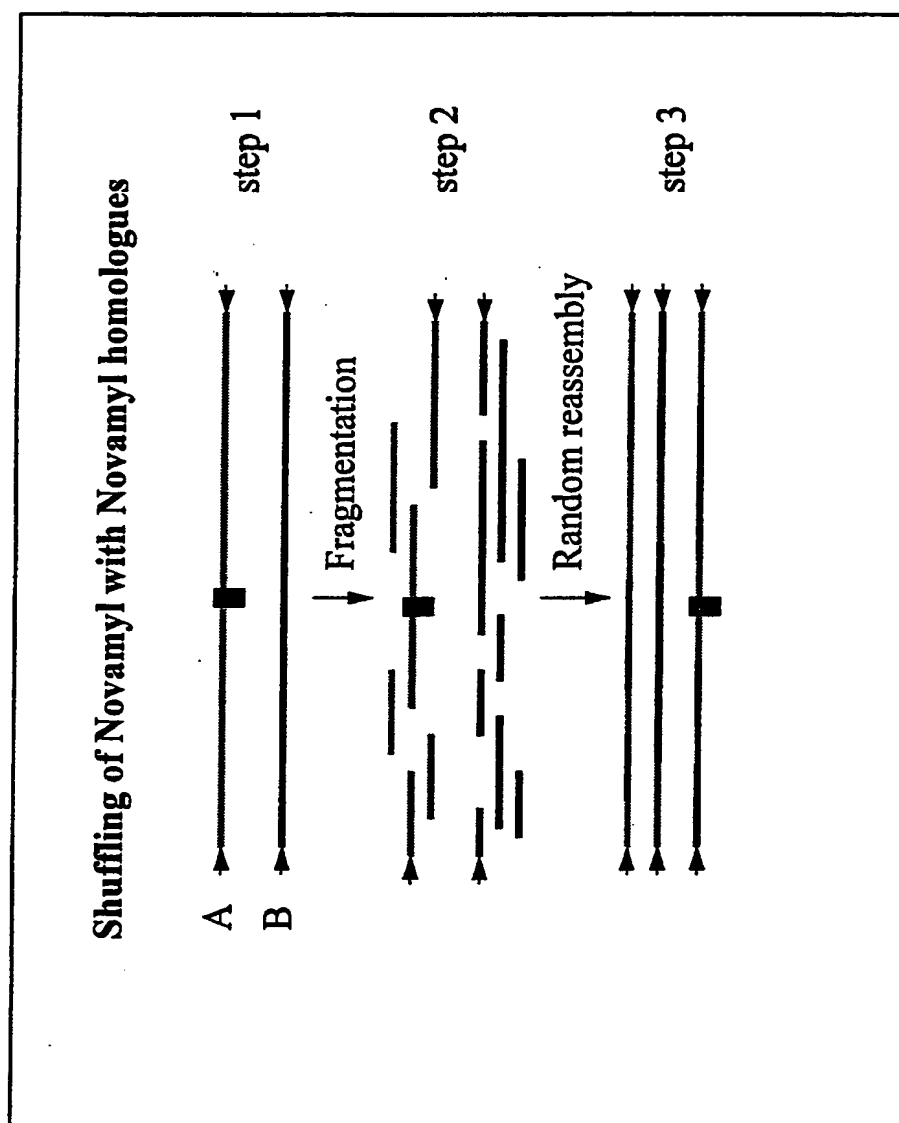


Fig. 2

3/5

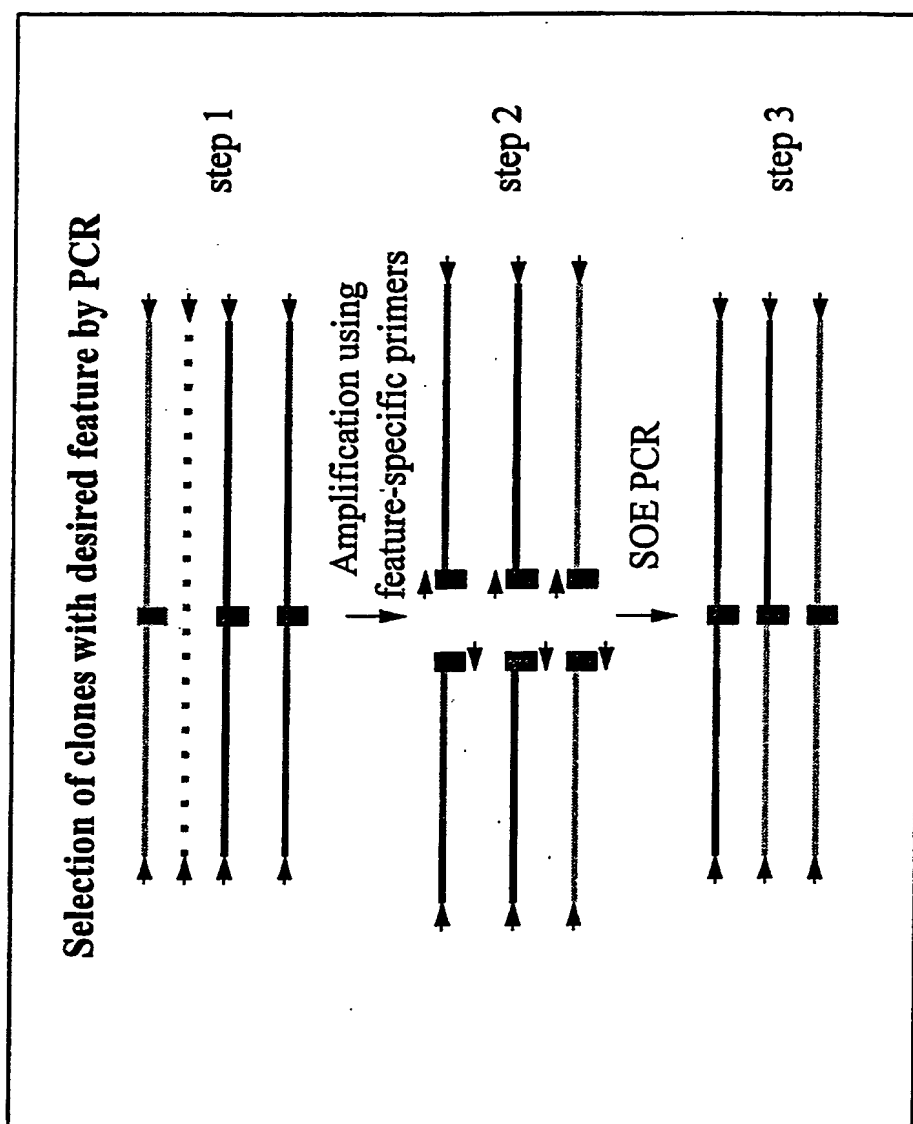


Fig. 3

4/5

1	10	20	30	40	50	60	70	80	
-----SSASVKG	DIYQII	IDRFYD	GD	TNNN	PAKSYG	LYDP	TSKWKW	YGGD	LEGVRQKL--PYLKQLGVTTI
ASDTAVSNV	NYSTDIYQ	IVTRFV	DGNTSNNPT	---	GDLYDP	THTS	SLKKYF	GGDWQGI	INKINDGYLTGMGVTAIWIS
APDTSVSNV	NYSTDIYQ	IVTRFV	DGNTSNNPT	---	GDLYDP	THTS	SLKKYF	GGDWQGI	INKINDGYLTGMGVTAIWIS
APDTSVSNKQNF	STDIYQ	IFTDRF	SDGNPANNPT	---	GAADF	GTCTN	RLRYCG	GDWQGI	INKINDGYLTGMGVTAIWIS
									72
									77
									77
									77
									148
PVLDN	DTLAGT	---	DNTG	HGYW	TRDFKQ	IEEH	FGNW	TTFD	TLVND
QPVENI	YAVLP	DS	T	FGG	STS	YHGY	WARD	FKRTN	PYFG
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QPVENI	YAVLP	DS	T	FGG	STS	YHGY	WARD	FKRTN	PYFG
									157
									157
									156
									228
LYNNG	TYMG	NYF	DD	ATK	GYF	HNG	DI	SNW	DDRYE
LYDNG	TLL	GGY	TNDT	-	NGYF	HHY	GGT	D	-
LYDNG	VLL	GGY	TNDT	-	NGYF	HHY	GGT	D	-
LYDNG	TLL	GGY	TNDT	-	QNL	FHNG	GGT	D	-
									230
									230
									229
									307
AVKH	NSG	FS	KS	L	AD	KLY	Q	KD	I
AVKH	MP	FG	WQ	KN	F	MDS	IL	SY	RP
AVKH	MA	FG	WQ	KN	F	MDS	IL	SY	RP
AVKH	MP	FG	WQ	KN	F	MDS	IL	SY	RP
									307
									306
									387
VNQ	T	G	N	E	Y	K	Y	K	E
I	Q	S	T	A	S	D	Y	N	F
I	Q	S	T	A	S	D	Y	N	F
LE	G	S	A	D	Y	A	Q	V	D
									386
									386
									386

Fig. 4

5/5

AFKEVSTILAGLRNNAAIQYGTTTQRWINNDVVIYERKFFENDVVLVA INRNTQSSYSISGLQTALPNGSYADYLSGLGG 467
 AXNVIKKLAPLRKSNPAIAYGTTQQRWINNDVVIYERKFGNNVALVA INRNLSTSYNITGLYTALPAGTYTDVLGGLNG 466
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 AYQVIQKLAPLRKCNPAIAYGSTQERWINNDVLIYERKFGSNVAVAVNRNLNAPASISGLVTSLPQGSYNDVLGGLNG 466

 NGISVS-NGSVASF TLAPGA VSVWQYST-SASAPQIGSVAPNMGIPGNVVTIDGKFGTTQGTVTFGGVTA T---VKSWT 543
 NSISVASDGSVTPPFTLSAGEVAVWQYVSSN-SPLIGHVGPTMTKAGQTITIDGRGFGTTSQVLFGSTAGT---IVSWD 542
 SSI TVSSNGSVTPPFTLAPGEVAVWQYVSTTN-PPLIGHVGPTMTKAGQTITIDGRGFGTTAGQVLFGTTPAT---IVSWE 542
 NTL SVSGGGAASNFTLAAGGTAVWQYTAATA-TPTIGHVGPMMAKPGVTITIDGRGFGSSKGTIVFGTTAVSGADITSWE 545

 SNRIEVYVPNMAAGLTDVKVTA-GGVSSNLYS-YNILSGTQTSVFTVKSAPPTNLGDKIYLTGNIPELGNWSTDTSGAV 620
 DTEVKVKVPSVTPGKYNISLKTSSGATSNYNNINILTGNOICVRFVNNASTVY-GENVYLTGNVAELGNWDTS----- 616
 DTEVKVKVPALT PGKYNITLKTASGVTSNYNNINVL TGNOVCVRFVNNATTVM-GENVYLTGNVAELGNWDTS----- 616
 DTQIKVKIPAVAGGNYNIKVANAAGTASNVDNFEVLSDQVSVRFVNNATTAL-GQNVYLTGVSVELGNWDPA----- 619

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 -KAIGPMFNQWVYQYPTWYDYDVSVPAGTTIEFKFIFKN--GSTVTWEGGYNHVYTTPTSGTATVIVDWQP 683
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Fig. 5

SEQUENCE LISTING

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<120> AMYLOLYTIC ENZYME VARIANTS

<130> 5241-WO, SLK

<140>

<141>

<160> 26

<170> PatentIn Ver. 2.0

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<211> 2160

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<220>

<221> CDS

<222> (1)..(2160)

<220>

<221> mat_peptide

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Met	Lys	Lys	Lys	Thr	Leu	Ser	Leu	Phe	Val	Gly	Leu	Met	Leu	Leu	Ile	
				-30				-25					-20			

ggt	ctt	ctg	ttc	agc	ggt	tct	ctt	ccg	tac	aat	cca	aac	gcc	gct	gaa	96
Gly	Leu	Leu	Phe	Ser	Gly	Ser	Leu	Pro	Tyr	Asn	Pro	Asn	Ala	Ala	Glu	
		-15				-10						-5				

gcc	agc	agt	tcc	gca	agc	gtc	aaa	ggg	gac	gtg	att	tac	cag	att	atc	144
Ala	Ser	Ser	Ser	Ala	Ser	Val	Lys	Gly	Asp	Val	Ile	Tyr	Gln	Ile	Ile	
-1	1				5				10					15		

att	gac	cgg	ttt	tac	gat	ggg	gac	acg	acg	aac	aac	aat	cct	gcc	aaa	192
Ile	Asp	Arg	Phe	Tyr	Asp	Gly	Asp	Thr	Thr	Asn	Asn	Asn	Pro	Ala	Lys	
			20				25						30			

agt	tat	gga	ctt	tac	gat	ccg	acc	aaa	tcg	aag	tgg	aaa	atg	tat	tgg	240
Ser	Tyr	Gly	Leu	Tyr	Asp	Pro	Thr	Lys	Ser	Lys	Trp	Lys	Met	Tyr	Trp	
			35				40					45				

ggc ggg gat ctg gag ggg gtt cgt caa aaa ctt cct tat ctt aaa cag 288
 Gly Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln
 50 55 60

ctg ggc gta acg aca atc tgg ttg tcc ccg gtt ttg gac aat ctg gat 336
 Leu Gly Val Thr Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp
 65 70 75

aca ctg gcg ggc acc gat aac acg ggc tat cac gga tac tgg acg cgc 384
 Thr Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg
 80 85 90 95

gat ttt aaa cag att gag gaa cat ttc ggg aat tgg acc aca ttt gac 432
 Asp Phe Lys Gln Ile Glu Glu His Phe Gly Asn Trp Thr Thr Phe Asp
 100 105 110

acg ttg gtc aat gat gct cac caa aac gga atc aag gtg att gtc gac 480
 Thr Leu Val Asn Asp Ala His Gln Asn Gly Ile Lys Val Ile Val Asp
 115 120 125

ttt gtg ccc aat cat tcg act cct ttt aag gca aac gat tcc acc ttt 528
 Phe Val Pro Asn His Ser Thr Pro Phe Lys Ala Asn Asp Ser Thr Phe
 130 135 140

gcg gaa ggc ggc gcc ctc tac aac aat gga acc tat atg ggc aat tat 576
 Ala Glu Gly Gly Ala Leu Tyr Asn Asn Gly Thr Tyr Met Gly Asn Tyr
 145 150 155

ttt gat gac gca aca aaa ggg tac ttc cac cat aat ggg gac atc agc 624
 Phe Asp Asp Ala Thr Lys Gly Tyr Phe His His Asn Gly Asp Ile Ser
 160 165 170 175

aac tgg gac gac cgg tac gag gcg caa tgg aaa aac ttc acg gat cca 672
 Asn Trp Asp Asp Arg Tyr Glu Ala Gln Trp Lys Asn Phe Thr Asp Pro
 180 185 190

gcc ggt ttc tcg ctt gcc gat ttg tcg cag gaa aat ggc acg att gct 720
 Ala Gly Phe Ser Leu Ala Asp Leu Ser Gln Glu Asn Gly Thr Ile Ala
 195 200 205

caa tac ctg acc gat gcg gcg gtt caa ttg gta gca cat gga gcg gat 768
 Gln Tyr Leu Thr Asp Ala Ala Val Gln Leu Val Ala His Gly Ala Asp
 210 215 220

ggt ttg cgg att gat gcg gtg aag cat ttt aat tcg ggg ttc tcc aaa 816
 Gly Leu Arg Ile Asp Ala Val Lys His Phe Asn Ser Gly Phe Ser Lys
 225 230 235

tcg	ttg	gcc	gat	aaa	ctg	tac	caa	aag	aaa	gac	att	ttc	ctg	gtg	ggg	864
Ser	Leu	Ala	Asp	Lys	Leu	Tyr	Gln	Lys	Lys	Asp	Ile	Phe	Leu	Val	Gly	
240					245					250					255	
gaa	tgg	tac	gga	gat	gac	ccc	gga	aca	gcc	aat	cat	ctg	gaa	aag	gtc	912
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Thr Val Thr Phe Gly Gly Val Thr Ala Thr Val Lys Ser Trp Thr Ser	
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Asn Arg Ile Glu Val Tyr Val Pro Asn Met Ala Ala Gly Leu Thr Asp	
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Val Lys Val Thr Ala Gly Gly Val Ser Ser Asn Leu Tyr Ser Tyr Asn	
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Pro Pro Thr Asn Leu Gly Asp Lys Ile Tyr Leu Thr Gly Asn Ile Pro	
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 Gln Gly Pro Leu Leu Ala Pro Asn Tyr Pro Asp Trp Phe Tyr Val Phe
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agc gtt cca gca gga aag acg att caa ttc aag ttc ttc atc aag cgt 2064
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Ala Ser Ser Ser Ala Ser Val Lys Gly Asp Val Ile Tyr Gln Ile Ile
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Ile Asp Arg Phe Tyr Asp Gly Asp Thr Thr Asn Asn Asn Pro Ala Lys
 50 55 60

Ser Tyr Gly Leu Tyr Asp Pro Thr Lys Ser Lys Trp Lys Met Tyr Trp
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Gly Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln
 85 90 95

Leu Gly Val Thr Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp
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Thr Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg
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Asp Phe Lys Gln Ile Glu Glu His Phe Gly Asn Trp Thr Thr Phe Asp
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Thr Leu Val Asn Asp Ala His Gln Asn Gly Ile Lys Val Ile Val Asp
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Phe Val Pro Asn His Ser Thr Pro Phe Lys Ala Asn Asp Ser Thr Phe
 165 170 175

Ala Glu Gly Gly Ala Leu Tyr Asn Asn Gly Thr Tyr Met Gly Asn Tyr
 180 185 190

Phe Asp Asp Ala Thr Lys Gly Tyr Phe His His Asn Gly Asp Ile Ser
 195 200 205

Asn Trp Asp Asp Arg Tyr Glu Ala Gln Trp Lys Asn Phe Thr Asp Pro
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Ala Gly Phe Ser Leu Ala Asp Leu Ser Gln Glu Asn Gly Thr Ile Ala
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Gln Tyr Leu Thr Asp Ala Ala Val Gln Leu Val Ala His Gly Ala Asp
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Gly Leu Arg Ile Asp Ala Val Lys His Phe Asn Ser Gly Phe Ser Lys
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Ser Leu Ala Asp Lys Leu Tyr Gln Lys Lys Asp Ile Phe Leu Val Gly
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Glu Trp Tyr Gly Asp Asp Pro Gly Thr Ala Asn His Leu Glu Lys Val
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Arg Tyr Ala Asn Asn Ser Gly Val Asn Val Leu Asp Phe Asp Leu Asn
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Thr Val Ile Arg Asn Val Phe Gly Thr Phe Thr Gln Thr Met Tyr Asp
 325 330 335

Leu Asn Asn Met Val Asn Gln Thr Gly Asn Glu Tyr Lys Tyr Lys Glu
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Asn Leu Ile Thr Phe Ile Asp Asn His Asp Met Ser Arg Phe Leu Ser
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Val Asn Ser Asn Lys Ala Asn Leu His Gln Ala Leu Ala Phe Ile Leu
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 450 455 460
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 610 615 620
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Glu Leu Gly Asn Trp Ser Thr Asp Thr Ser Gly Ala Val Asn Asn Ala
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Gln Gly Pro Leu Leu Ala Pro Asn Tyr Pro Asp Trp Phe Tyr Val Phe
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Ser Val Pro Ala Gly Lys Thr Ile Gln Phe Lys Phe Phe Ile Lys Arg
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<210> 15
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<223> Description of Artificial Sequence: Primer A91

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gatcccggga ctgccaacca tgtaaataat acgtattttg c

41

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 99/00087

A. CLASSIFICATION OF SUBJECT MATTER

IPC6: C12N 9/28, A21D 8/04

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC6: C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	Dialog Information Service, File 155, Medline, Dialog accession no. 09574180, Medline accession no. 98316627, Wind RD et al: "Engineering of factors determining alpha-amylase and cyclodextrin", Eur J Biochem (GERMANY) May 1 1998, 253 (3) p598-605	7-10,12-21, 23-25
	--	
X	WO 9633267 A1 (NOVO NORDISK A/S), 24 October 1996 (24.10.96), page 4, line 1 - line 9; page 7, line 17 - line 19; page 53, line 16 - line 19	7-10,12-21, 23-25
A	--	11



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

7 June 1999

Date of mailing of the international search report

08 -06- 1999

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 99/00087

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Dialog Information Service, File 155, Medline, Dialog accession no. 07301145, Medline accession no. 92111781, Nakamura A. et al: "Functional relationships between cyclodextrin glucanotransferase from an alkalophilic Bacillus and alpha-amylases. Site-directed mutagenesis of the conserved two Asp and one Glu residues", FEBS Lett (NETHERLANDS) Jan 13 1992, 296 (1) p37-40 --	17-21
A	File WPI, Derwent accession no. 89-312221, OJI CORNSTARCH KK: "Increasing amylase activity of CGT ASE gene - to carboxy terminal side of cyclo-maltodextrin glucano: transferase", JP,A,1228475, 880912, DW8943 --	7-21,23-25
A	Biochemistry, Volume 33, 1994, Akira Nakamura et al, "Four Aromatic Residues in the Active Center of Cyclodextrin Glucanotransferase from Alkalophilic Bacillus sp. 1011: Effects of Replacements on Substrate Binding and Cyclization Characteristics", page 9929 - page 9936, See page 9229 left column, line 15-22 --	1-25
A	EMBL, Databas GenBank/DBJ, accession no. E02907, Udaka J. et al: "Enzymatic Gene Having Raw Starch Decomposition Activity And Cyclodextrin Synthetic Activity, Recombinant DNA Containing the Gene, VECTOR, Transformant, Production of the Enzyme Using The", & JP 1991123491-A/1, 1991-05-27 --	1-6
A	Databas Swissprot, accession no. P19531, Diderichsen B. et al: "Maltogenic Alpha-Amylase Precursor (EC 3.2.1.133) (GLUCAN 1,4-Alpha-Maltohydrolase", FEMS MICROBIOL. LETT. 56:53-60 (1988), 1991-02-01 --	1-6
X	 --	22

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 99/00087

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>Dialog Information Service, File 357, Derwent Biotechnology Abs, Dialog accession no. 0173836, DBA accession no. 95-00657, Agency-Ind.Sci.: "Saccharomycopsis fibuligera alpha-amylase or Bacillus macerans cyclomaltodextrin-glucanotrans- ferase mutant preparation - enzyme engineering for improved production of oligosaccharide", JP,A,6253836, 940913, 325-327</p> <p>--</p>	1-25
A	<p>Plant Molecular Biology, Volume 25, 1994, Birte Svensson, "Protein engineering in the alpha-amylase family: catalytic mechanism, substrate specificity, and stability" page 141 - page 157</p> <p>--</p>	1-25
A	<p>Biochemistry, Volume 34, 1995, Dirk Penninga et al, "Site-Directed Mutations in Tyrosine 195 of Cyclodextrin Glycosyltransferase from Bacillus circulans Strain 251 Affect Activity and Product Specificity" page 3368 - page 3376</p> <p>--</p>	1-25
A	<p>STN International, File CAPLUS, CAPLUS accession no. 1994:477140, Document no. 121:77140, Demchuk, Eugene et al: "Modeling of the 3D structure of Bacillus circulans var.alkalophilus cyclomalto- dextrin glucanotransferase and comparison with alpha amylase", Mol. Modell., 9th (1993), Meeting Date 1992, 433-4</p> <p>-- -----</p>	1-25

INTERNATIONAL SEARCH REPORT

Information on patent family members

03/05/99

International application No.

PCT/DK 99/00087

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9633267 A1	24/10/96	AU 5396896 A	07/11/96
		CA 2217876 A	24/10/96
		EP 0822982 A	11/02/98
<hr/>			